



1

SEQUENCE LISTING

<110> ITOH, NOBUYA  
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING 3-HYDROXYCYCLOHEXANONE

<130> Q76481

<140> 10/617,034

<141> 2003-07-11

<150> JP 2002-205207

<151> 2002-07-15

<160> 15

<170> PatentIn Ver. 3.2

<210> 1

<211> 348

<212> PRT

<213> Corynebacterium pseudodiphtheriticum

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			20					25					30		
Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro
		35					40					45			
Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly
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Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile
65					70					75					80
Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Asn	Cys	Trp
			85						90					95	
His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu
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Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe
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Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp
	130					135					140				
Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His
145					150					155					160
Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val
				165					170					175	

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg  
 180 185 190  
 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys  
 195 200 205  
 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp  
 210 215 220  
 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala  
 225 230 235 240  
 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala  
 245 250 255  
 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly  
 260 265 270  
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu  
 275 280 285  
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
 290 295 300  
 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr  
 305 310 315 320  
 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly  
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 Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu  
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 <212> DNA  
 <213> Corynebacterium pseudodiphtheriticum

<220>  
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 gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96  
 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val  
 20 25 30  
 acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144  
 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro  
 35 40 45

gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly 50 55 60	192
gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile 65 70 75 80	240
gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp 85 90 95	288
cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu 100 105 110	336
gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe 115 120 125	384
atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp 130 135 140	432
ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His 145 150 155 160	480
gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val 165 170 175	528
gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg 180 185 190	576
cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys 195 200 205	624
ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp 210 215 220	672
aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala 225 230 235 240	720
gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala 245 250 255	768
atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly 260 265 270	816

gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864  
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu  
 275 280 285  
 gct tcg gtg aca gtc ccg tat tgg ggt gcc cgc aac gag ttg atc gaa 912  
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
 290 295 300  
 ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc tcg gtg gag acc 960  
 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr  
 305 310 315 320  
 ttc agt ctc gac aac ggt gcc gaa gcg tat cga cga ctg gct gcc gga 1008  
 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly  
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 <211> 325  
 <212> PRT  
 <213> *Penicillium citrinum*

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 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp  
 35 40 45  
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg  
 50 55 60  
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val  
 65 70 75 80  
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp  
 85 90 95  
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met  
 100 105 110  
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu  
 115 120 125  
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 130 135 140  
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<220>  
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<222> (1)..(978)
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1				5					10					15		
ggc	gtc	ggc	ttt	ggg	acc	ttc	gct	agt	gaa	ggg	tcc	aag	ggc	gag	acc	96
Gly	Val	Gly	Phe	Gly	Thr	Phe	Ala	Ser	Glu	Gly	Ser	Lys	Gly	Glu	Thr	
			20					25					30			
tat	act	gct	gtc	acc	act	gcc	ctg	aag	acc	ggg	tac	cgt	cac	ttg	gac	144
Tyr	Thr	Ala	Val	Thr	Thr	Ala	Leu	Lys	Thr	Gly	Tyr	Arg	His	Leu	Asp	
		35					40					45				

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Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
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Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
245 250 255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
260 265 270	

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 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp  
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ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912  
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val  
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 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala  
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<220>  
 <223> Description of Artificial Sequence: Primer

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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

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<210> 7  
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 <212> DNA  
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<220>  
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<210> 8  
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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

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&lt;210&gt; 9

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 9

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21

&lt;210&gt; 10

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 10

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21

&lt;210&gt; 11

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Bacillus megaterium

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&lt;222&gt; (1)..(786)

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Met	Tyr	Lys	Asp	Leu	Glu	Gly	Lys	Val	Val	Val	Ile	Thr	Gly	Ser	Ser	
1				5				10					15			

acc	ggt	tta	gga	aaa	gca	atg	gcg	att	cgt	ttt	gcg	aca	gaa	aaa	gct	96
Thr	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Ala	Thr	Glu	Lys	Ala	
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aaa	gta	gtt	gtg	aac	tat	cgt	tcg	aaa	gaa	gaa	gaa	gct	aac	agc	gtt	144
Lys	Val	Val	Val	Asn	Tyr	Arg	Ser	Lys	Glu	Glu	Glu	Ala	Asn	Ser	Val	
		35				40					45					

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Leu	Glu	Glu	Ile	Lys	Lys	Val	Gly	Gly	Glu	Ala	Ile	Ala	Val	Lys	Gly	
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65 70 75 80	
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa	288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	
aat ccg gtt tct tct cat gaa atg tct tta agt gat tgg aat aaa gtc	336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val	
100 105 110	
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att	384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tct	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
130 135 140	
agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
caa gca gga cgc gga taa	786
Gln Ala Gly Arg Gly	
260	

&lt;210&gt; 12

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Bacillus megaterium

&lt;400&gt; 12

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Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
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Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
          35          40          45

Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50          55          60

Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65          70          75          80

Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
          85          90          95

Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
          100          105          110

Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
          115          120          125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
          130          135          140

Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
          145          150          155          160

Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
          165          170          175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
          180          185          190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
          195          200          205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
          210          215          220

Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
          225          230          235          240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
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Gln Ala Gly Arg Gly
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&lt;210&gt; 13

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

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<220>  
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<212> DNA  
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<220>  
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